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Sequence 92, Appl Sequence 114, App Sequence 119, App Sequence 110, App Sequence 109, App Sequence 114, App Sequence 116, App Sequence 126, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 142, App Sequence 16, Appli Sequence 12, Appli Sequence 12, Appli Appli Sequence 12, Appli Appli Appli Sequence 12, Appli Ap
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(c) 1993 - 2006 Compugen Ltd.
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US-08-818-112-114
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US-10-103-002-109
US-10-103-002-106
US-09-073-010-126
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US-09-287-849-26
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US-08-818-111-106 US-09-056-556-111 US-09-072-596-110 US-09-072-596-110 US-08-072-967-111 US-08-084-843-111 US-08-084-843-111 US-08-095-734-2 US-08-471-869-2 US-08-471-869-2 US-08-471-869-2 US-08-471-869-2 US-08-411-1104 US-09-075-556-109 US-09-072-596-109 US-09-072-596-109 US-09-072-596-104 US-09-072-596-104	ALIGNMENTS K BS FRAGMENTS M M. TUBERCUL 09/050,739 6/97 7/97 7/97	Mycobacterium tuberculosis 92 100.0%; Score 1892; DB 2; Length 371; imilarity 100.0%; Pred. No. 1.4e-154; Conservative 0; Mismatches 0; Indels 0; Gaps MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWT MITMLWHAMPPELNTARLMAGAGPAPWLAAAAGWQTLSAALDAQAVELTARLNSLGEAWT MITMLWHAMPPELNTARLMAGAGPAPWLAAAAGWQTLSAALDAQAVELTARLNSLGEAWT GGGSDKALAAATPWVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQA
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00000000000000000000000000000000000000	739-92 92, Application US/0 0. 6641814 INFORMATION: NT: ANDERSEN, PETER NT: NIELSEN, Rikke NT: OFTINGER, Thomat NT: ROSHKRANDS, Ida NT: ROSHKRANDS, Ida NT: PROSHKRANDS, Ida NT: PROSHKRANDS, Ida NT: PROSHKRANDS, Ida NT: PROSHKRANDS, Ida NT: PROSHCSEN, Retion NT: PROSHCSEN, Retion NT: PLONIO, WILLEIC F INVENTION: DRILEIC F INVENTION: DRILEIC F ILING DATE: 1997-04 APPLICATION NUMBER: FILING DATE: 1997-04 APPLICATION NUMBER: FILING DATE: 1997-04 APPLICATION NUMBER: FILING DATE: 1997-04 FILING DATE: 1997-04 APPLICATION NUMBER: FILING DATE: 1997-06 F SEQ ID NOS: 173 B: PATENTING DATE: 1998-07 OF SEQ ID NOS: 173 B: PATENTING DATE: 1998-07 OF SEQ ID NOS: 173	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Campoe-Neto, Antonia
APPLICANT: Campoe-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIE: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210121.417C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 109, Application US/08818111; Patent No. 638852; GENERAL INFORMATION; GENERAL APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 2101
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
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CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 368;
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,112

FILING DATE: 13-MAR-1997

CLASSIFICATION: 42-0-1

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.411C6

TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%; Score 1873; DB 2;
99.7%; Pred. No. 6e-153;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114, Application US/08818112
Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 anino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and E
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STRANDEDNESS: si
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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STATE: Washingt
COUNTRY: USA
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TOPOLOGY:
US-08-818-112-114
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                                                     SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT 123
STINPIFGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Romald C.
TITLE OP INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-WAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 109, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101;
TELEPHONIC (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
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STREET: 63
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US-09-072-596-109
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                                            SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT 123
                                                                                                              ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPWASILDPGASQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 114, Application US/09056556
; Batent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STRET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Scattle
STATE: Washington
COUNTY: COLUMBIA
                                                                                                                               GGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
        1 MLWHAMPPEXNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998
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ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 21015
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 367; Conserva
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US-09-056-556-114
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121 ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQ 180
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                                                                                                                                                                                                                                                                                                                                                                                 64 SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQ
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                                                                                                                                                                                                                                                                                              4 MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
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                                                                                                                                                                                                               Length 368;
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STATE: Washington
COUNTRY: USA
ZIP: 981.04-7092
COMPUTER READABLE FORM:
WEDIUM TYPE: FIDEDBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 Fifth Avenue
                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                           Score 1873; DB 2
Pred. No. 6e-153;
0; Mismatches
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND ME.
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 109, Application US/10193002
Patent No. 6949246
GENERAL INFORMATION:
               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
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                                                                                : 368 amino acids
amino acid
                                                                                                                                                                                                                                 Best Local Similarity 99.7
Matches 367; Conservative
                                                                                                                          STRANDEDNESS: single
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DWDEEDDW 368
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US-09-072-967-114
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US-10-193-002-109
                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                124 ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASO 183
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                                                                                                                                                      1 MIWHAMPPEXNTARIMAGAGPAPWILAAAAGWQTLSAALDAQAVELTARINSIGEAWTGGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                        181 STTNPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                          4 MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGNPADBEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
                                                                                     Gaps
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                     ;
0
                                         99.0%; Score 1873; DB 2; Length 368; 99.7%; Pred. No. 6e-153;
                                                                                Indels
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                                                                                   0; Mismatches
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 114, Application US/09072967
Patent No. 6592877
                                                             Best Local Similarity 99.7
Matches 367; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washingt
COUNTRY: USA
US-09-072-596-109
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EXPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED 363
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                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FOROM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
               Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1873; DB 2;
Pred. No. 6e-153;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMOUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-084-843-114
BERRY LLP
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; Sequence 126, Application US/09073009
Patent No. 6555653
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 368 amino acids
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 114
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.0%;
Best Local Similarity 99.7%;
Matches 367; Conservative
 ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J
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                                CITY: Seattle
STATE: Washington
COUNTRY: USA
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Vedvick, Thomas S.
Twardaik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
ALILE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                            99.0%; Score 1873; DB 2; Length 368;
99.7%; Pred. No. 6e-153;
ive 0; Mismatches 1; Indels
                                                       PRIOR CARSAFEATION:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTONED APER: 05-MAY-1998
ATTONED ARE: 05-MAY-1998
ATTONED MAKE: MAKE, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-631
INFORMATION POR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
           APPLICATION NUMBER: US/10/193,002
                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 109: US-10-193-002-109
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APPLICANT: Reed, Steven G.
Billon, Davin C.
Campos-Neto, Antonio
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Patent No. 6962710
GENERAL INFORMATION:
                            FILING DATE: 10-Jul-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                    LENGTH: 368 amino acids
                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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Matches 367; Conservative
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GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMFOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 ALAAATPMVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLTATN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 FFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDP----- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 FGTPNFPTSISALLTDLÓPYASXXYNTEGLPYFSIGMGNNFIQSÁKTLGLIGSAAPAAVA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 LAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQL----IEK-----PVAPSVMP 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 MAEAVAPYVAWMSAAAAQAEQAATQARAAAAAFAAFAATVPPPLIAANRASLMQLISTN
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30.6%; Pred. No. 2.7e-23;
tive 39; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,010
FILING DATE: 05-MAY-1998
                                                                                                                                            210121.440C1
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 126:
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206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.6*
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                     98104
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                                                                         TUBERCULOSIS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 FFGINTIPIALTEMDYFIRMWQAALAMEVYQAETAVNTLFEKLEPMASILDP----- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 AAVATAAGTAQSTLIEMIIGLEN------ALQSLISXLLQSSNGPLSWLWQIL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 FGTPNFPTSISALLTDLQPYASXXYNTEGLPYFSIGMGNNFIQSAKTLGLIGSAAPAAVA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 AAGDA-----AKGLPGLGGMLGGGPVAAGLGNAASVGKLSVPPVWXGPLPGSVTP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 MAEAVAPYVAWMSAAAAQAEQAATQARAAAAFEAAFAATVPPPLIAANRASLMQLISTN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 VFGONTSAIAAAEAQYG-EMWAQDSAAMYAYAGSSASASASAVTPFSTPPQIANPTAQGTQA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 -----GASQST-TNPIFGMPSPGSSTPVGQLPPAATQTLGQ--LGEMSGPMQQLTQ-- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 -------PLQQVTSLFSQVGG----TGGGNPADEEAAQMGLLGTSPLSNHP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 LAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQL----IEK-----PVAPSVMP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ALPPEVNSVRMYAGPGSAPMVAAASAWNGLAAELSSAATGYETVITQLSSEGWLGPASAA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 AA-----TRP---GLVAPA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 GAAPLPVSTVSAAPEAAPGSLLGGLPLXGAGGAGAGPRYGFXPTVMARPPFXGIVAAA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAWTGGGSDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%; Score 366; DB 2; Length 40. 30.6%; Pred. No. 2.7e-23; ive 39; Mismatches 153; Indels
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05-MAY-1998
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campode-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
ADDRESSEE: SEED and BERRY
                                                                                                                                                                6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 206-622-6901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 126: SEQUENCE CHARACTERISTICS: LENGTH: 400 amino acids TYPE: amino acid sTRANDEDNESS: aingle TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.6%
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                             98104
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; Sequence 126, Application US/09073010

RESULT 10 US-09-073-010-126

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APPLICANT: Alderson, Mark
APPLICANT: Campos Netc, Antonio
APPLICANT: Campos Netc, Antonio
APPLICANT: Campos Netc, Antonio
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Title Uses
TITLE OF INVENTION: And Title Uses
TITLE OF INVENTION: And Title Uses
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT FILIG DATE: 1998-12-30
SUTHER T APPLICATION NUMBER: US/09/223,040
SUTHER T APPLICATION NUMBER: 100
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 28.9%
Matches 120; Conservative
                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 NFFGINTIPIALTEMDYFIRMWQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQST 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 NWFGONTPALATTESQY-AEMWAQDAAAMYGYASAAA------PATVLTPFA--- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------PPPQTTNATG-LVGHATAVAALRGQHSWAAAIPWSDIQKYWMMFLGALATAEG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 FIYDSGGLTLNALQFVGGMLWSTALAE---AGAAEAAAGAG------GAAG----WSA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSQLIEKPVAPSVMPAAAG--SSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 KALAAATPMVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEA--WTGGGSD
                                                                                                                    APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward H.
ITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
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                                                                                                                                                                                                                                              TITLE OF INVENTION: INTERACTIONS OF PROTEINS FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR PELING DATE: 2000-11-28
PRIOR FILING DATE: 2000-02-01
PRIOR PLING DATE: 2000-02-01
PRIOR PLING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
                                  Sequence 205, Application US/09712363 Patent No. 6892139
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Matches 120; Conserv
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Sequence 2, Application US/09223040 Patent No. 6544522 GENERAL INFORMATION:

-09-223-040-2

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213 GQLGEMSGPMQQLTQPLQQVTSLFSQVGG--TGGGNPADEEAAQMGLLGTSPLSNHPLAG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Mycobacterium tuberculosis Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 IATNILIGONTPALAVNEAEYG-EMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFEKLEPMASILDPGASQSTINPI-----FGMPSPGSSTPVGQL-----PPAATQTL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTGG-TTPSSKLGGLWKTVSPHRSPIS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 GSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIBKPVAP-----SVMPAAAAGSSAT 322
                                                                                                                                                                                                                                                                                                                                                    63 GSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVL 122
                                                                                                                                                                                                                                                                                        8 AMPPELNTARLMAGAGPAPMLAAAAGWQTL----SAALDAQAVELTARLNSLGEAWTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 GGAAPVGAGAMGQGAQSGG-----STRPGLVAPAPLAQEREED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-223-040-2
                                                                                                                                                                                                  77;
                                                                                                                                               Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 TATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNT----
                                                                                                                                                                                                  Indela
                                                                                                                                            ; Score 330.5; DB 2;
; Pred. No. 6.8e-20;
45; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycol
TITLE OF INVENTION: Quantum Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US/08/942,578
PRIOR APPLICATION NUMBER: US/08/942,578
PRIOR PLING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US/08/942,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Autonio
APPLICANT: Corixa Corpozation
TITLE OF INVENTION: Pusion Protiens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09287849
Patent No. 6627198
GENERAL INFORMATION:
                                                                                                                                                 17.5%;
28.9%;
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1999-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                         GSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 SAGLMVAAASPYVAMMSVTAGOAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 IATNILIGONTPAIAVNEAENG-EMWAQDAAAMFGYAAATATATLLIPFEEAPEMTSAGG 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: : | : | : | : | 322 LLEQAAAVEEASDTAAAANQLMNVVPQALQQLAQQLAQG-TTPSSKLGGLWKTVSPHRSPIS 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | : | | | : | | 381 NWVSMANNHWSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSSLGSSLGSS 440
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                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-2
                                                                                                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                                                                                                               Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 TATNFFGINTIPIALTEMDYFIRMWNQAALAMBVYQAETAVNT-----
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17.5%; Score 330.5; DB 2;
Best Local Similarity 28.9%; Pred. No. 6.8e-20;
Matches 120; Conservative 45; Mismatches 173;
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PRIOR PELING DATE: 1997-03-13
PRIOR PELING DATE: 1997-03-13
PRIOR PELING DATE: 1997-10-01
PRIOR PELING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PELING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1998-04-07
PRIOR PELLING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 729
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Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 TATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNT----
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MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.4%; Score 328.5; DB 2; 28.9%; Pred. No. 7.7e-20; tive 45; Mismatches 173;
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APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
AITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
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Patent No. 6555653
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-12-30
                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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                                     NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver.
SEQ ID NO 26
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STREET: 6300
TTW: Seattle
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                                                                                                                                                                                LENGTH: 596
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 QSTINPIFGMPSPGSSTPVGQLPP-----AATQTLGQLGEMS--GPMQQLTQ 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 DEPERHWGPFGGAAPVSAGVGHAALVGALSVPHSW--TTAAPEIQLAVQ--ATPFFSSSA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 AAATQAAGAGAVADAQATLAQLPPGILSDILSALAANADPLTSGLLGIASTLNPQVGSAQ 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 MPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAWTGGGSDKA 67
                                                                                                                                                                                                                                                                                                                                              Query Match 17.2%; Score 326; DB 2; Length 423;
Best Local Similarity 30.4%; Pred. No. 7.9e-20;
Matches 121; Conservative 45; Mismatches 164; Indels 68; Gaps
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMULTORION INFORMATION:
TELEPLA: 206-622-4900
TELEPLA: 206-682-6031
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-073-009-142:
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
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seq length: 200000000
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                                                                                                 January
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                  OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                  Searched:
                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	_	Aay21946 Amino aci		_	Aaw32384 Mycobacte	Aaw32452 Mycobacte	Aaw64338 Mycobacte	Σ	Σ	Σ	-	_	_	_	Pro	Aaw73654 M. tuberc	Aaw73764 M. tuberc	_	Abu34103 Protein e	_	_	Abu34048 Protein e	Aag81154 Mycobacte	Adz36102 Mycobacte
SUMMARIES		ព	AAW72929	AAY21946	AAB19844	ADG15733	AAW32384	AAW32452	AAW64338	AAW81705	AAY38992	AAY39135	ABU05362	ADG15750	ABU34364	AAB66451	ABU36905	AAW73654	AAW73764	AAU08225	ABU34103	ABM15864	ABU36014	ABU34048	AAG81154	ADZ36102
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	* Query	Match	100.0	100.0	99.3	99.3	0.66	0.66	99.0	99.0	0.66	99.0	27.9	26.5	23.1	22.8	22.8	19.3	19.3	19.3	19.2	19.1	18.8	18.8	18.2	18.1
		Score	1892	1892	1878	1878	1873	1873	1873	1873	1873	1873	527	502	436.5	430.5	430.5	366	366	366	363.5	362	356	355.5	344.5	343
	Result	No.		8	m	4	Ŋ	•	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

Claim 1; Page 200-202; 163pp; English.

Ada26373 Mycobacte Aae29708 Mycobacte Aae17572 Mycobacte		4000		Ada26366 Mycobacte Ada26365 Mycobacte Aae29731 Mycobacte Ada26364 Mycobacte Ada26370 M. bovis
ADA26373 AAE29708 AAE17572	AUF69/53 ADA26356 ADA26368 AAY32070	AAE17574 ADF69777 AAU74599	AAC22142 AAE29709 AAE17573 ADA26374 ADA26367	ADA26366 ADA26365 AAE29731 ADA26364 ADA26370
729 7 729 5 729 5	1010 7 11154 7 596 2 596 2 596 2	2000 2000 2000 2000 2000	729 5 729 5 729 7 729 7	825 7 875 7 930 5 930 7
17.6	17.1 17.5 17.4 1.7 1.4	17.4	17.1 17.4 17.4 4.7.1	4.7.1 4.7.1 4.7.7 4.4.4
333.5 330.5	330.5 330.5 328.5	328.5 328.5 328.5	322832	328 328 328 328 328 5 328 5
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ALIGNMENTS

Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen; New isolated mycobacteria polypeptides and nucleic acids - used for developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis. Rasmussen PB; Andersen P, Nielsen R, Rosenkrands I, Weldingh K, Oettinger T, Florio W; Mycobacterium tuberculosis antigen RD1-ORF5 AAW72929 standard; protein; 371 AA 97DK-00000376. 97US-0044624P. 97DK-00001277. 98WO-DK000132 98US-0070488P Mycobacterium tuberculosis. (STAT-) STATENS SERUM INST (first entry) WPI; 1998-542705/46. N-PSDB; AAV63939 02-APR-1997; 18-APR-1997; 10-NOV-1997; 05-JAN-1998; 21-JAN-1999 01-APR-1998; WO9844119-A1 08-OCT-1998 infection AAW72929; AAW72929 us-09-872-505a-6.rag

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The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment (II) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from Mr tuberculosis protein ESAT-6, or MFT59 and a second different amino acid sequence from Mr tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo compared to post-translational processing; (3) a mucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or brovious sensitization in an animal with bacteria belonging or tuberculosis complex. The invention also describes the use of CFP7A or CFP10A. The invention also describes the use of CFP7A or CFP10A. The invention also describes the use of CFP7A or esponse in a mammal; use of CFP7A, CFP19 or MPT59-ESAT6, cresponse in a mammal; use of CFP10A, CFP19 or MPT59-ESAT6, cresponse in a mammal; use of CFP10A, CFP19 or MPT59-ESAT6, cresponse in a mammal; use of CFP10A, CFP19 or MPT59-ESAT6, cresponse in a mammal; use of CFP10A, CFP19 or MPT59-SAT6, cresponse in a mammal; use of CFP10A, CFP19 or MPT59-SAT6, cresponse of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and cell epitope of for the preparation of an immunological composition; and companies of the composition of a subunit vaccine
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; Pred. No. 2.2e-131;
0; Mismatches 0;
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Example 2; Page 219-220; 265pp; English
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Best Local Similarity 100.0%;
Matches 371; Conservative 0
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tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A, CFP30A;
CFP7B, CFP19; CFP27; CFP30A; RDI-ORF; CFP10A; CFP16; CFP19; CFP23;
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                                                                                                                           Length 371;
                                                                                                                                                                                                       Indels
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                                                                                                              Score 1892; DB 2;
Pred. No. 2.2e-131;
Mismatches 0;
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-DK000438
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEDDWDEEDDW 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-347282/29.
N-PSDB; AAX81046.
                                                                                                                                                             Similarity
                                          Sequence 371 AA
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                                                                                                                                                                                               Matches 371;
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                                                                                                                  Query Match
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antibacterial; antitubercular; tuberculostatic; vaccine;
diagnostic reagent; epitope; RD1 region; RD2 region;
Mycobacterium tuberculosis; Mycobacterium bovis; Mycobacterium africanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic reagents comprising a peptide having an epitope from polypeptides Rv1986, Rv3878, Rv1983, Rv3873 or Rv3879 derived from RD1 and RD2 regions of Mycobacterium, useful as vaccines against
                                                                        M tuberculosis Rv3873 protein for generating peptide epitopes
                                                                                                                                                                                                                                                                                                                                                     (UKEN-) UK SEC FOR ENVIRONMENT FOOD & RURAL AFF
                                                                                                                                                                                                                                                                        28-APR-2003; 2003WO-GB001815.
                                                                                                                                                                                                                                                                                                        27-APR-2002; 2002GB-00009723
                                                                                                                                                                                                                                                                                                                     27-APR-2002; 2002GB-00009724
                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium infections.
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                                                                                                                                                                                                         WO2003093307-A2.
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                                                                                                                                                                                                                                                                                                                                                                                         Cockle PJ,
             ADG15733;
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                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of the Mycobacterium tuberculosis MTBN3 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AAB19842-49), encoded by 8 open reading frames (see AAB9015-4-2) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. MTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic vaccination methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                         Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.3%; Score 1878; DB 4; L
100.0%; Pred. No. 2.3e-130;
ive 0; Mismatches 0;
                                                                                                                                                               (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 1; 35pp; English.
                                                                                                2000WO-US012257
                                                                                                                             99US-0132505P
   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 368; Conservative
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                                                                                                                                                                                                                                                N-PSDB; AAA89037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 368 AA;
                                 WO200066157-A1
                                                                                                                                04-MAY-1999;
                                                                                                04-MAY-2000;
                                                                  09-NOV-2000
                                                                                                                                                                                                Gennaro ML;
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                                      The invention relates to a novel diagnostic reagent comprising a peptide epitope from a protein encoded by the RD1 or RD2 regions of the Mycobacterium tuberculosis, M. bovis or M. africanum genome. The diagnostic reagents comprised within the kit are selected so that they are able to differentiate between M. bovis, M. tuberculosis or M. africanum-infected mammals and mammals vaccinated against M. bovis, M. tuberculosis or M. africanum. The polypeptide or its variant or fragment is useful as a medicament provided that the polypeptide is not a MpT-64 polypeptide or a polypeptide encoded by the RV1984c region of the M. bovis, M. tuberculosis or M. africanum genomes. The nucleic acid which encodes the polypeptide or the diagnostic reagents can be used as a vaccine, especially against Mycobacterium infections. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT
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Pred. No. 2.3e-130;
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100.0%; Pred. No. a...
Claim 19; SEQ ID NO 5; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 368; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 368 AA;
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ADG15733 standard; protein; 368 AA.

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22-SEP-1995;
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Vedvick TH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M tuberculosis antigen, Tb37-FL. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antibodies, are especially monoclonal antibodies or equivalent polyclonal antibodies, are
                                                        360
EKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED
                                   EKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                                                                                                                                                                                                        Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%; Score 1873; DB 2;
99.7%; Pred. No. 5.5e-130;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen Tb37-FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 159-161; 190pp; English
                                                                                                                                                                                                                                                                                                                                       /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                               AAW32384 standard; protein; 368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon DC,
DR;
                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00523435.
95US-00532136.
96US-00620280.
96US-00658800.
96US-00680573.
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                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                          (first entry)
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                                                                               DWDEEDDW 371
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DWDEEDDW 368
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           Misc-difference
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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Vedvick TH,
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tuberculosis, also for
SDKALAAATPWVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT
                                                                                     124 ATNPFGINTIPIALTEMDYFIRMWQAALAMEVYQAETAVNTLFEKLEPMASILDPGASO
                                                                                                      ATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLBPMASILDPGASQ
                                                                                                                                                                                                    241 GGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
                                     SDKALAAATPWVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT
                                                                                                                                       STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                                                             181 STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                                                                                                                                        EKPVAPSVMPAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogen; vaccine; tuberculosis; non specific adjuvant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen Tb37-FL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             AAW32452 standard; protein; 368 AA.
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DR;
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95US-00533634.
96US-00620874.
96US-00659683.
96US-00680574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skin testing; M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis.
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I, Twardzik
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A new immunogenic polypeptide has been developed comprising

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Matches 367; Conservative

4 MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG

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                                                                                                                                                         SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT 123
                                                                                                                                                                                         ATNFFGINTIPIALTEMDYFIRMWOAALAMEVYQAETAVNTLFEKLEPWASILDPGASQ 183
immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, Th37-FL The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                          63
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                                                                                                                                   STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
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                                                                                                                          4 MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                          Gaps
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                                                                                          Length 368;
                                                                                                          Indels
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                                                                                         Score 1873; DB 2;
Pred. No. 5.5e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis; infection; diagnosis; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen Tb37-FL.
                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unidentified"
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97US-00818111.
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                                                                                           99.0%;
99.7%;
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                                                                                                           367; Conservative
                                                                                                                                                                                                                                                                                                                                            368
                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
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                                                                                                  Local Similarity
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Misc-difference
                                                                           Sequence 368 AA;
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09-NOV-1998
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                                                             prevention)
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Matches
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STINPIFGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                         This polypeptide comprises Mycobacterium tuberculosis antigen Tb37-FL. I is encoded by genomic DNA isolated from a M. tuberculosis strain H37Rv genomic library using a probe from clone Tb38-1 (see AAV4384). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising man antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                 New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
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  Houghton
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  Dillon DC, Campos-Neto A, DR, Lodes MJ;
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99.7%; Pred. No. 5.5e-130;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                   Example 3; Page 143-144; 250pp; English.
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     Skeiky YAW,
Twardzik
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                                                                                 WPI; 1998-251292/22.
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Vedvick TS,
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AAY38992 standard; protein; 368

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKPVAPSVMPAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                               Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing protective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLWHAMPPEXNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
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                                                                                                                                                                                                                                              Houghton R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1873; DB 2;
Pred. No. 5.5e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Example 3B; Page 137-138; 230pp; English.
                                                                                                                                                                                                                                              Dillon DC, C
                                      Location/Qualifiers
                                                                 /label= unknown
                                                                                                                                                 97WO-US018293
                                                                                                                                                                           96US-00730510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.7%;
Matches 367; Conservative
              Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis of tuberculosis
                                                                                                                                                                                                                                                         Twardzik
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DWDEEDDW 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 368 AA;
                                                    Misc-difference
                                                                                                                                                                           11-OCT-1996;
13-MAR-1997;
                                                                                            WO9816646-A2
                                                                                                                                                 07-OCT-1997;
                                                                                                                                                                                                                                                           Vedvick TS,
                                                                                                                    23-APR-1998
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                                                                                                                                                                                                                                              SG,
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SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STINPI FGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                    M.
current
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLWHAMPPEXNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel recombinant antigens and their encod nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as cur vaccination strategies do not provide 100% immunity
                                                                                        diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                         tuberculosis
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                                                                                                                                                                                                                                                                                 Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                     Σ̈́
                                                                  M. tuberculosis recombinant antigen protein Tb37-FL
                                                                                                                                                                                                                                                                                Campos-Neto A, J, Hendrickson
                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising antigenic portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1873; DB 2;
Pred. No. 5.5e-130;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 177-179; 323pp; English.
                                                                                                                                                                                                                                                                                Skeiky YAW, Dillon DC, Ca
3, Twardzik DR, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.04;
                                                                                                                                                                                                99WO-US003265
                                                                                                                                                                                                                       98US-00024753
98US-00072596
                                                                                                                            Mycobacterium tuberculosis
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.7
Matches 367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWDEEDDW 371
                                                                                                                                                                                                                                                                                                                  WPI; 1999-527416/44.
                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                      immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 368 AA;
                                                                                                                                                                                                17-FEB-1999;
                                                                                                                                                 WO9942118-A2
                                             05-NOV-1999
                                                                                                                                                                                                                       18-FEB-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                                                            Vedvick TS,
                                                                                                                                                                          26-AUG-1999
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                                                                                          Antigen,
                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                 Reed SG,
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EKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED
          GGNPADEEAAOMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLI
                                                                                                                                                                                                                                                                                                                                                                               Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.
                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis and M. leprae marker protein #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 176; 874pp; English.
                                                                                                                                                                                                                                                     ABU05362 standard; protein; 302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2002; 2002WO-IB001973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-2001; 2001US-0270123P
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.1
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method of the invention
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DWDEEDDW 368
                                                                                                                                        DWDEEDDW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-759885/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200274903-A2.
                                                                                                                                                                                                                                                                                                                    08-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2002.
                                                                                                                                                                                                                                                                                       ABU05362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19299 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLWHAMPPEXNTARLMAGAGPAPMLAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATWFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTNPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STITVPIEGMPSPGSSIPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                   Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                          M. tuberculosis antigen Tb37-FL amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1873; DB 2;
Pred. No. 5.5e-130;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 132-133; 299pp; English.
                                                                             AAY39135 standard; protein; 368 AA
                                                                                                                                                                                                                                                                                                                                                                      99WO-US003268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                      98US-00025197
98US-00072967
                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.7
Matches 367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
DWDEEDDW 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 368 AA;
                                                                                                                                                                                                                                                                                                          WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                        17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1998;
05-MAY-1998;
                                                                                                                                             05-NOV-1999
                                                                                                                                                                                                                                                                                                                                        26-AUG-1999
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361
                                                                                                           AAY39135;
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                                                                                                                                                                                                                                                                  This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Mycobacterium leprae identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%; Score 527; DB 5; Length 302;
45.1%; Pred. No. 1.1e-30;
ive 31; Mismatches 78; Indels
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Gaps

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Length 100 Indels

Score 502; DB 7; Pred. No. 2.1e-29;

Query Match 26.5%; Score 502; DB Best Local Similarity 100.0%; Pred. No. 2.1 Matches 100; Conservative 0; Mismatches

151 9

1 ATAQAAAYTQAMATTPSLPEIAANHITQAVLTATNFFGINTIPIALTEMDYFIRMWNQAA 92 ATAQAAAYTQAMATTPSLPEIAANHITQAVLTATNFFGINTIPIALTEMDYFIRMWNQAA

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152 LAMEVYQAETAVNTLFEKLEPMASILDPGASOSTTNPIFG 191

LAMEVYQAETAVNTLFEKLEPMASILDPGASQSTTNPIFG

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ABU34364 standard; protein; 445

RESULT 13 ABU34364 ID ABU

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258
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                                         181
                                                          152 LTSQVNQFTQMISGFSAALPSTQVLQ-----QTVGQVAE-----LARPMQQVKSLFT 198
                                                                                                                                                                                         OVGGTGGGNPAD----EEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; antitubercular; tuberculostatic; vaccine;
diagnostic reagent; epitope; RDI region; RD2 region;
Mycobacterium tuberculosis; Mycobacterium bovis; Mycobacterium africanum.
39 IAAAKPMITWLQSA-----AEQTTTQAEAHRQAMASTPGMAVITENHITQAILATINF 91
                                                                                                                                                                                                                                                                 294 TRIPLMS--QLIEKPVAPS-----VMPAAAGSSATGGAAPVGAGAMGQGAQSGGST 343
                                                                                                                                                                                                                                                                                       New diagnostic reagents comprising a peptide having an epitope from polypeptides Rv1986, Rv3878, Rv1983, Rv3873 or Rv3879 derived from RD1 and RD2 regions of Mycobacterium, useful as vaccines against
                                         FGINTIPIALTEMDYFIRMWQAALAMEVYQAETAVNTLFEKLEPMASILDPGA----
                                                                                                               --SQ--STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFS
                                                                                                                                                                                                                            199 SIDSTGVYTSAQRGDTESAHRIGLFGASTLSSHPLVGITGTTTDTRLLCAESLPSASGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hewinson RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence fragment used to generate epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UKEN-) UK SEC FOR ENVIRONMENT FOOD & RURAL AFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 23; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon SV,
                                                                                                                                                                                                                                                                                                                                                                                                ADG15750 standard; protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-2003; 2003WO-GB001815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002GB-00009723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cockle PJ, Vordermeier HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-903652/82.
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27-APR-2002;
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Mycobacterium bovis.

WO200277183-A2.

03-OCT-2002

Protein encoded by Prokaryotic essential gene #19891.

(first entry)

19-JUN-2003

ABU34364;

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the nucleic acid inhibits proliferation of a cell. Also included are:

the 6213 antiennes sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

cof the nucleic acid inhibits proliferation of a cell. Also included are:

cof the nucleic acid; (2) a host cell containing the vector; (3) an isolated

concleic acid; (2) a host cell containing the vector; (3) an isolated

colypeptide or its fragment whose expression is inhibited by the

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide (5) producing the polypeptide; (6) inhibiting cellular

contriberation or the activity of a gene in an operon required for

proliferation or the activity of a gene in an operon required for

corporated for proliferation, (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway of

corporated for proliferation, or that inhibits cellular proliferation or the biological

contentifying a gene required for cellular proliferation or the biological

contentifying a proliferation-required gene or its gene product lies

corporated activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 62288; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029926/02.
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method of the invention.

Sequence 100 AA;

Zyskind JW; Xu HH;

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Ohlsen | Forsyth |

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

ņ, Wang

21-MAR-2001; 2001US-0081E242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P.

21-MAR-2002; 2002WO-US009107

2002US-00072851

08-FEB-2002;

06-MAR-2002; 2002US-0362699P

(BLIT-) BLITRA PHARM INC. Zamudio C, Trawick JD,

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12;
to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational for dury discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. arreus, S. typhimurium, R. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis; attenuated microorganism; Rv3018c;
signature tagged transposon mutant; mutant library;
mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTATNFFGINTIPIALTEMDYFIRMWQAALAMEVYQAET-AVNTLFEKLEPMASILDPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIIGFIITLASNAQLLTE--FAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLLGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGGAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                     GGSDKALAAATPWVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 PSAELFVAAYVPYVAWLVQASADSAAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLIGA-----LAAAVVPGVAG-----LAGVAGLAAVPAVGAAAGAPAALVGSVA 354
                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                                                                                                        14 TPVWLASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSAVVAAVGAGVWQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 QTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGNPADEEAAQMGLLGTSPLSNH
                                                                                                                                                                                                                                                                                                                                             3 TMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AWTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ANEASNAVAAATITPFPWHEIVOFLEETFAAYDQYLSALLSELPAVAWVWFQLFVDILGF
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                          Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Mycobacterium tuberculosis Rv3018c gene.
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASQ----STTNPI-----FGMPSPGSSTPVGQLPPAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Mismatches 155;
                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                        23.1%; Score 436.5; DB 6
33.6%; Pred. No. 8.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB66451 standard; protein; 434 AA
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.6%
Matches 133; Conservative
                                                                                                                                                                                                                                          Sequence 445 AA;
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08-JUL-1999;
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The present sequence is given in a specification relating to a method for screening a library of mutants. The method comprises constructing a library with insertions in genes and/or regulatory regions of the coganisms of interset, where the insertion contains a teg and/or a coganisms of interset, where the insertion contains a teg and/or a cransposon associated with a tag. The mutants are identified by transposon associated with a tag. The mutants are identified by creating an individual suffering from a mycobacterial infection, suspected of being infected with a Mycobacterium, or having been exposed to an infectious Mycobacterium. It is also useful for identifying and isolating mutants of actinomycetales and for identifying compounds that have antibiotic activity. The method is used to identifying and microorganisms, preferably an actinomycetales, such as M. tuberculosis, C. microorganisms, preferably an actinomycetales, such as M. tuberculosis, m. leprae, M. avium, M. intracellulaire and M. tuberculosis, consecuing vaccines. The method can be used to screen constructing vaccines. The method can be used to screen consecuing vaccines. The method can be used to screen conditions or different strains of the same organism. The present procein is encoded by a gene which is disrupted by the insertion of the IS 1096 transposon to produce an attenuated mutant of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 OGPSAELFVAAYVPYVAWLVQASADSAAAGEHEAAAAGYVCALAEMPTLPELAANHLTH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGANEASNAVAAATITPFPWHEIVQFLEETFAAYDQYLSALLSELPAVAWVWFQLFVDIL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGNPADEEAAQMGLLGTSPLS 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 GFNIIGFIITLASNAQLLTE--FAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening a mutant library for mutants unable to grow under specific conditions and for identifying loci involved in pathogenicity, comprises using signature tagged transposon mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGASQ----STTNPI------FGMPSPGSSTPVGQLPPAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 VAPVSCGVVSPQARLVSAVEP---APASTSVSVLASDR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
22.8%; Score 430.5; DB 4;
Best Local Similarity 33.2%; Pred. No. 2.4e-23;
Matches 132; Conservative 45; Mismatches 158;
                                                                                                                                                                                                                                                           Example 8; Fig 20A; 159pp; English
                                                             Camacho L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU36905 standard; protein; 434
                                                             Guilhot C,
                    (INSP ) INST PASTEUR
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                                                                                                                             N-PSDB; AAF31607
                                                             Gicquel B,
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요
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63; Gaps

45; Mismatches 158; Indels

Matches 132; Conservative

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the inventor fractate to an interact acts to where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid containing the vector;

(2) a vector comprising a promoter operably linked to the nucleic acid;

(3) a host cell containing the vector;

(3) an isolated containing the vector;

(3) an isolated containing the vector;

(4) an antibody capable of specifically binding the polypeptide or is fragment whose expression is inhibited by the antisense nucleic acid;

(5) producing the polypeptide;

(6) proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or equired for proliferation, or that inhibits cellular proliferation;

(8) the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation;

(8) the gene product or that the proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts;

(9) manufacturing an antibiotic;

(10) profiling a compound that inhibits the gene or a gene on which the test compound that inhibits the compound activity;

(11) a culture comprising strains in which the gene product is overexpressed or underexpressed;

(12) determining the extrains is present in a culture or collection of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational contended for proliferation to isolate candidate molecules for rational contended for proliferation are screening homologous nucleic acids

(11) a contended for proliferation in cells other than S. aureuses, S. typhimiumium, experiments and the proposed proversors and the present seminary of the present of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WiPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
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Forsyth RA,
                                                                                                                Protein encoded by Prokaryotic essential gene #22432
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 64829; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072881.
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                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                  (first entry)
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Trawick JD,
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N-PSDB; ACA40775.
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                                                                  19-JUN-2003
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                   ABU36905
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Wall
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6; Length 434;

Score 430.5; DB 6 Pred. No. 2.4e-23;

22.8%; 33.2%;

Query Match Best Local Similarity

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178
                                                                                               180 PGANEASNAVAAATITPFFWHEIVQFLEETFAAYDQYLSALLSELPAVAWVWFQLFVDIL 239
                                                                                                                                                                                                                                                                                             264
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59
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                                                                        60 TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ
                                                                                                                                               AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD
                                                                                                                                                                                                                                                                                                                    240 GFNIIGFIITLASNAQLLTE--FAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLL
1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AW
                                                                                                                                                                                                                                                                                             209 -TQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVG---GTGGGNPADEEAAQMGLLGTSPLS
                                                                                                                                                                                                                                                                                                                                                                      265 NHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGG
                                  1 MTAPVWLASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGAGVW
                                                                                                                                                                                                                      PGASQ----STINPI-----FGMPSPGSSTPVGQLPPAA-----
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STRAIN=CDC 1551 / Obhkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
PDCI=10.1128/JB1.84.19.5479-5490.2002;
Fleichmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gavinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.E., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Praser C.M.;
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J. Bacteriol. 184:5479-5490(2002).
BEBRI, ARCOOSIG; AAK48355.1; -; Genomic_DNA.
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Length 371,
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Pfam; PR0823; PPE; 1.
SEQUENCE 371 AA; 37686 MW; CC25F5865131C79B CRC64;
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99.7%; Pred. No. 4.3e-98;
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OrderedLocusNames=MT3987;
Mycobacterium tuberculosis.
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                         GTGGGNPADEBAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMS
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EMBL; BX248347; CAD96089.1; -; Genomic_DNA.

InterPro; IPR000039; Microbac_PPE.
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N 6=PPB68; OrderedLocusNames=MD3903;
M 50bacterium bovis.

Edacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0T-2004 (TrEMBLrel. 26, Last annotation update)
PPL FAMILY PROFESIN.
NG-EPPE68, OrderedLocusNames=WD3903;
M.Cobacterium bovis.
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MEDLINE-9829597; PubMed=9634230; DOI=10.1038/31159;
MEDLINE-98295987; PubMed=9634230; DOI=10.1038/31159;
MEDLINE-98295987; PubMed=9634230; DOI=10.1038/31159;
MEDLINE-98295987; PubMed=96.34230; DOI=10.1038/31159;
Harris D.E., Gordon S.V., Elglmeier K., Gas S., Barry C.E. III,
Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Kroph A., McLean J., Moule S.,
Murphy L.D., Oliver S., Seeger K., Skelton S., Squares S., Squares S.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Mature 393:537-544(1998).
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                                                                                                                                                                                 Name=PPE68; OrderedLocusNames=Rv3873;
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae;
Corymebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.3%; Score 1878; DB 2; Length 368; Best Local Similarity 100.0%; Pred. No. 1.4e-97; Matches 368; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 AA; 37330 MW; D78F44095F658CA2 CRC64;
                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
PPE FAMILY PROTEIN
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Tubercullist; RV3873; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PP00823; PPE; 1.
MYCTU PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 LTSQVNQFTQMISGFSAALPSTQVLQ-----QTVGQVAE-----LARPMQQVKSLFT 198
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MEDLINE-IN,
MEDLINE-IN,
MEDLINE-IN,
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Cole S.T., Eiglmeier K., Parkhill J., Churcher C.M., Harris D.B.,
Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B.,
Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Stevens K., Simon S., Simmonds M., Skelton J., Squares Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Gaps
                                                                                                                                                                                                                                                                               Biglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.; "Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae.";
                                                                                                                                           Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 302;
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SEQUENCE 302 AA; 32135 MW; EDAC4CCOAF3BF3D0 CRC64;
                                                             01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annocation update)
Hypothetical protein MLCB628.14c (PPB-family protein)
Name-MLCB628.14c; OrderedLocusNames=ML0051;
                                                                                                                                                                                     Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
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EMBL; AL583917; CAC29559.1; -; Genomic_DNA.
                                            Created)
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InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                       MEDLINE=93188700; PubMed=8446027;
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                                          01-JAN-1998 (TrEMBLrel. 05,
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O33085_MYCLE PRELIMINARY;
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                                                                                                                                                                                                        NCBI_TaxID=1769;
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                                                                                                                                                                                                                                                                                                                          MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

EMBL; BX248344; CAD96734.1; -; Genomic_DNA.

Proc. DATE PRO00030; Microbac_PPE.
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical PPB-family protein PPB47/PPB48.
Name-ppe47/ppe48; OrderedLocusNames=Rv3021c/Rv3022c, MT3106;
ORFNames=MTV012.35c/MTV012.36c;
                                                                                                                                                                         Bācteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 AA; 42878 MW; 62A5615EB0D0DEED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 GGAAPVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 GSVAPVSGGVVSPQARLVSAVEP---APASTSVSVLASDR 377
                                                                   Last sequence update)
Last annotation update)
                                                              update)
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435 AA
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                                                                                                                                Name=PPE47; OrderedLocusNames=Mb3047C;
                                            Created)
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                                         (TrEMBLrel. 25, C
(TrEMBLrel. 25, I
(TrEMBLrel. 26, I
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MYCBO PRELIMINARY;
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                                                                                                                                                           Mycobacterium bovis.
                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                             PPE FAMILY PROTEIN
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                                                                                                                                                                                                                                                  NCBI_TaxID=1765;
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                                            01-OCT-2003
                                                                   01-OCT-2003
                                                                                      01-MAR-2004
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PGANEASNAVAAATITP---FPFGELAKFLEMAAQAFTEVGELIMKSAEAWAVGFVELIT 236
                                                                                                               237 GLVNFEPWLVLTGMIDMFFATVGFALGVFVLVPLLEFAVVLELAILSIGWIISNIFGAIP 296
                                                                                                                                                       LSNHPLAGGSGPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSAT 322
                                                                                                                                                                                            297 VLGGPLLGA------LAAAVVPGVAG------LAGVAGLAALPAVGAAAGAPAALV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPBIAANHITQAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTATNFFGINTIPIALTEMDYFIRMWNQAALAMBVYQAET-AVNTLFEKLEPMASILDPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 NIIGFIITLASNAQLLTE--FAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLLGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLAGGSGPSAGAGILRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGGAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AWTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 PSAELFVAAYUPYVAMLVQASADSAAAGEHEAAAAGYVCALAEMPTLFELAANHLTHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ASQ-----STINPI-----FGMPSPGSSIPVGQLPPAA-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 OTLGOLGEMSGPMOOLTQPLQQVTSLFSQVG---GTGGGNPADBEAAQMGLLGTSPLSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garnier T., Eigimeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkinil J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; Proc. Omplete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S., A. 100:7877-7882(2003).

EMBL, BZ248344, CAD96730.1; -; Genomic_DNA.

Interpro; IPR000030; Microbac_PPB.

Fram, PF00823; PPB; 1.

Complete proteome.

437 AA, 43383 MM; 2B295898155009D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Mismatches 155; Indels
PGASQSTTNPIFGMPSPGSSTPVGQLP---PAATQTLGQLGEM---
                                                                                                                                                                                                                                                                          341 GSVAPVSGGVVSPQARLVSAVEP---APASTSVSVLASDR 377
                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                          ----OPLOQVISL----FSQVG---GTGGGNPADEEAAQM-
                                                                                                                                                                                                                                       GGAAPVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 23.1%; Score 436.5; DB 2 Local Similarity 33.6%; Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=PPE46; OrderedLocusNames=Mb3043c;
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                              Q7TXF8 MYCBO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPE FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=AF2122/97;
                                     180
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179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITO 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVLTATNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                MEDIZIRE=9925987; PubMed=9634230; DOI=10.1038/31159;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Haris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornbby T., Jagels K., Kroph A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTAPVWLASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGAGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22206494; PubMed=12218036; MEDLINE-22206494; PubMed=12218036; DOI-10.1128/JB.194.19.5479-5490.2002; DOI-10.1128/JB.194.19.5479-5490.2002; Peterson J.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.P., Nolson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to a
Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.3%; Score 440; DB 1; Length 435; Best Local Similarity 33.5%; Pred. No. 6.9e-17; Matches 134; Conservative 51; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 184:5479-5490(2002).
-!- SIMIGARITY: Belongs to the mycobacterial PPE family.
-!- CAUTION: Ref.1 Bequence differs from that shown due frameshift in position 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
299 G -> A (in Ref. 2).
320 LAGV -> VTGL (in Ref. 2).
326 L -> V (in Ref. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BX842581; CAES5541.1; ALT FRAME; Genomic_DNA.
EMBL; BX842581; CAES5542.1; ALT_FRAME; Genomic_DNA.
EMBL; AE000516; AAK47435.1; -; Genomic_DNA.
                  Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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435 AA, 42877 MW;
                                                                                                                                                                                                                                                                                                                                                           Nature 393:537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuberculist; Rv3021c; -. Tuberculist; Rv3022c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
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CONFLICT
SEQUENCE
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TIGR;
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209

61 65

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63;

Length 437;

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laboratory
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SO WERE REPORTED TO THE PROPERTY OF THE PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVLTATNFFGINTIPIALTEMDYFIRMWNQALAMEVYQAETAVNTLFEKLEPMASILDP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AALQATNFFGINTIPIAVNEADY-ARMWVQAATTWTTYQ---AVSTAAVAATPQ-TMPAP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVTSLFSQVGGTGGGNPADEEAAQMGLLGTSPLSNHPLAGG-----SGPSAGAGLLRAE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AVTSIGAAAGAAGG-----LVGLAGLA--SPGPLPTGAEMVPVTAPPPGATPAPTA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404
    ---LAGVAGLAAVPAVGAAAGAPAALVGSVA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 PLIGGPASAPATIPVSSAAAAPTAPAPAVAAAGSAAPPPAGPGGFPYLVGGMRVSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGSDKALAAATPWVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0-----TOPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 ANLAGTPAKLAQIFSNPSVLFSWPTLLWVLDFIAGRIFDILVTLKFLLEQPLLYVVGLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kapur V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 518;
                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017240; AAS06275.1; -; Genomic_DNA.
InterPro, IPR000030; Microbac_PPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 AA; 52170 MW; BAC863B26F9CCF62 CRC64;
                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.9%; Score 432.5; DB 2; 32.6%; Pred. No. 2.2e-16;
                                            PVGAGAMGQGAQSGGSTRPGLVAPAP----LAQER 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Mismatches 155;
                                                                                 347 PVSGGVVSPQARLVSAVEP---APASTSVSVLASDR
                                                                                                                                                                                   518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 AA
        PLLGA-----LAAAVVPGVAG----
                                                                                                                                                                                                                          Created)
                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                        Mycobacterium paratuberculosis.
                                                                                                                                                                                                                    05-JUL-2004 (TEMBLrel. 27, 05-JUL-2004 (TEMBLrel. 27, 15-JUL-2004 (TEMBLrel. 27, 14) TOUT-2012 (TEMBLrel. 27, 14) TOUT-101 protein. OrderedLocusNames=MAP3725;
                                                                                                                                                                               O73TJ3 MYCPA PRELIMINARY;
Q73TJ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
SEQUENCE 518 AA
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1770;
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P31500; 053265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=k10;
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          303
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CDC 1551 / Oshkosh;
MEDLINE22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Haftey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99295987; PubMed=9634230; DOI=10.1038/31159;
MEDLINE=99295987; PubMed=9634230; Garnier T., Churcher C.M., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Takris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Ollver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares S., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; But B. Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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Patki A.H., Dale J.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
--- SIMILLARITY: Belongs to the mycobacterial PPB family.
--- CAUTION: In strain Oshkosh the gene for this protein is interrupted in position 307 by an IS6110 element.
--- CAUTION: Was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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434 AA; 43029 MW; 41D673C4BD389DD6 CRC64;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical PPE-family protein PPE46.
Mame=ppe46; OrderedLocusNames=Rv3018c, MT3098/MT3101;
ORFNames=MTV012.32c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BX842581; CAES5538.1; -; Genomic_DNA.
EMBL; AE000516; AAK47427.1; ALT_SEQ; Genomic_DNA.
EMBL; AE000516; AAK47430.1; ALT_SEQ; Genomic_DNA.
EMBL; XS9271; CAA41861.1; ALT_FRAME; Genomic_DNA.
PIR; E70857; E70857.
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Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strains."
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=1773;
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DB 1, Length 434;

22.8%; Score 430.5;

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51787 MW; E8FBEB74E2F578E1 CRC64;
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InterPro; IPR000030; Microbac_PPB.
Pfam; PF000823; PPB; 1.
Complete proteome.
SEQUENCE 513 AA; 51787 MW; RAF
                                                                                                              PGASOSTINPIFGMPSPGSSTP.
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Nature 393:537-544(1998).
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Q7DA35; Q6MX52;
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                                                                                                                                                       TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ 119
                                                                                                                                                                                   120 AVLTĄTNFFGINTIPIALTEMDYFIRMWNQAALAMEVYQAET-AVNTLFEKLEPMASILD 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 GGPLLGA------LAAAVVPGVAG------LAGVAGLAALPAVGAAAGAPAALVGS 341
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                                                                1 MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGE-AW
                                                                                           PGASQ-----STTNPI-----FGMPSPGSSTPVGQLPPAA-----
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                         Gaps
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EMBL; BX248335; CAD93158.1; -; Genomic_DNA.
                      63;
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                      Indels
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Last annotation update)
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                      45; Mismatches 158;
Pred. No. 2.3e-16;
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01-OCT-2003 (TrEMBLrel. 25, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
PPE FAMILY PROTEIN
Name=PPE4; OrderedLocusNames=Mb0294;
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis complex
33.2%;
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Q7U2C9;
                      Matches 132; Conservative
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Complete proteome.
SEQUENCE 513 AA: 517
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Best Local Similarity
Similarity
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120 AVLTATIVEFGINTIPIALTEMDYFIRMWNOAALAMEVYQAET-AVNTLFEKLEPMASILD 178
                                                      PGGGAAST-----VGAVNPWQWLLALLQQLWNAYTGFYGWMLQLIWQFLQDPIGNSI 231
                                                                                                                                                                                                                                                                                                                                                  -----LTOPLOOVTS------LFSQVGGTGGGNPADEEAAQMGLLGTSPLSNH 266
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PTWGMILSSPFL-L 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAGGSGPSAGAGL---LRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 PAGLGLGLAAIAFLPIVLAPAVIPPAS-----TPLAAAAV---AAGSVWPAV---SMAVT 328
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STRAIN=H37Rv;
MREDLINE=9829587; PubMed=9634230; DOI=10.1038/31159;
Cole S.T., Barosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Comnor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares S.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22206494; PubMed=12218036; MEDLINE=22206494; PubMed=12218036; DOI=10.1128/JB.184.19.5479-5490.2002; Peteschmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDEDDW 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 GAGTAGAATPAAGAAPSAGAAPAPAPATASFAYAVGGSGDW 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             PPE family protein.
Name=PPE4; OrderedLocusNames=MT0299, Rv0286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000516; AAK44523.1; -; Genomic_DNA
EMBL; BX842573; CAE55266.1; -; Genomic_DNA
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306 PVAPSVMPAAAAGSSATGGA-APVGAGAM------GQGAQSGGST--RPGLVAPAPLA 354
127 GALVATNFFGINTIPIAVNEADY-ARMWVQAAGTWATYQAVSTAAVAAVPQPDPAPSILK 185
                                                                                                                                           Q-----QVTSLFSQVGGTGGGNPA-
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                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 AVLTATNPEGINTIPIALTENDYPIRMWNQAALAMBVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                                                                                                                                                                                                          121 TVLVATNPFGINTIPITLINEADY-VRMMIQAAAVMGLYQAASGAALASAPRTVPAPTVMN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 KIIIAFLTNPIQALITYGPLLFALGYQIFFNLVGW-------PTWGMILSSPFL-L 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 PLAGGSGPSAGAGL---LRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                     TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAYTQAMATTPSLPBIAANHITQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LIQPLQQVTS-----LFSQVGCTGGGNPADEEAAQMGLLGTSPLSNH 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 PGGGAAST-----VGAVNPWQWLLALLQQLWNAYTGFYGWMLQLIWQFLQDPIGNSI
                                                                                                                            MITMLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAW
                                                                                                                                                                       1 MAAPIWMASPPEVHSALLSNGPGPGSLVAAATAWSQLSAEYASTAABLSGLLGAVPGWAW
                                                                                 Gaps
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                                 Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li L., Baniantine J., Zhang Q., Amonsin A., Alt D., Kapur Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017239; AAS06640.1; -; Genomic_DNA.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 531 AA; 53742 MW; B392FE119582DC8C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                               44; Mismatches 155;
                                   DB 2;
                                   Score 430.5; DB:
Pred. No. 2.8e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                      22.8%;
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Best Local Similarity 34.9%
Matches 137; Conservative
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                                                                                 134; Conservative
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                                                              Similarity
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1073 U78

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60 TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPBIAANHITQ 119 61 EGPTTEAYVAAHAPYLAWLDQSSADAAGEAAQHEIAASAYTVALATWPTLPELATNHATH 120 AVLTATINFFGINTIPIALTEMDYFIRWWNQAALAMBVYQAETAVNTLFEKLEPWASIL-- 177 121 AALVATNFFGINTIPIALNEADY-ARMWVQAATTMSTYQ---TVSTSTLAAAPRSSAAPA 176 227 QTLGQLGE-----MSGPMQQLTQPLQQVTSLFSQVGGTGGGNPADEEAAQMGLLGTSPLS 264 265 NHPLAGGSGPSAGAGLLRA-------ESLPGAGGSLTRTPLMSQLIEK 305 272 FVGLAGLAGLAGLAPAPEPVPATVADVPAPTSPPNQALPVAGIPSASTPAS----- 325 -----DPGAS------CSTTNPIFGMPSPGSSTPVGQLPPAAT 209 NHPLAGGSGPSAGAGLIRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAA--GSSAT 322 245 ...-DERAAQM-GLLGTSP-LS 264 246 DPLWWVVRALELFSDFQQFGALLQENPAARQFITELVLLDWPTHLAQLASWLPTQPQLL 305 9 177 IVKSEDSSAGDTGDSSGGGGFFGDLLSAWENFVMNLMDQLFGVDSP------PDLAS 228 AVAAFLANPSPALFSALLFALAYEIAFDTLFFSPV-------ALLAAPFLP 1 MITWLWHAMPPELNTARLMAGAGPAPMLAAAAGWOTLSAALDAQAVELTARLNSL-GBAW |: | | :: | | :: | | STAAHDHDDHEHGDDHDHGFDSPLNQFVAQILRLFGIDWDPVEGTLNGLPYEAYTSPA PGASQSTTNPIFGMP----SPGSSTPVGQLPPAATQTLG-----QLGEMSG-PMQQLTQPL Indels 103; Kapur V.; Hypothetical protein.
OrderediocusNames=MAP3737;
Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteria, Actinobacteria, Corynebacterines; Mycobacterines; Mycobacterines; Mycobacteriaces; Mycobacterium; Mycobacterium avium complex (MAC). DB 2, Length Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL, ASG017240; ASG06287.1; -; Genomic_DNA. InterPro; IFR000030; Microbac_PPE. Pfam; PP00823; PPE; 1. Complete proteome, Hypothetical protein. SEQUENCE 504 AA; 49761 MW; 4DD3E220EB495932 CRC64; Created)
Last sequence update)
Last annotation update) Query Match 22.4%; Score 423.5; DB 2; Best Local Similarity 32.9%; Pred. No. 6.8e-16; Matches 138; Conservative 39; Mismatches 140; 353 AGATPIAASA----AASGPAPAP---TPAPTA 377 GGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLA 354 504 AA

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TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 OLGEMSGPMQQLTQPLQQVTSL-FSQVGGTGGGNPADEEAAQMGLLGTSPLSNHPLAGGS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPVLPGVAAAPSGGGAAAVLAPGPGASAATVSPAPAPAGMPATAPAPVGPPTPPPATGV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 GPSAGAGLLRAESLPGAGGSLTRTPLMSQLIEKPV-APSVMPAAA-----AGSSA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 WAGE---SLLYFTPOVPQLTQLSFGLIA-----PPIPAAGAPGVAGLAGLAGGA-LAGGA
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017230; AA503461.1; -; Genomic_DNA.
InterPro; IPR000030; Microbac_PPE.
Pfan, PF00823; PPE; 1.
Complete proteome.
SEQUENCE 488 AA; 48598 MW; C2FD0FB977DE334B CRC64;
                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Mycobacteriaceae, Mycobacterium,
Mycobacterium avium complex (MAC).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
07-deredLocuaNames=MAP1813.5;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridee;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 488;
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                                                                                                                      Last sequence update)
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                                                                              Q741E7_MYCPA PRELIMINARY;
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Q73YZ0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 QVTSLFS---QVGGTGGGNP----ADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLL 281
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      179 APGAEAGAATAAAVQSAAAAPATDSGSNINHADTSSIQQQASTAAQSYPSWQDQLTAWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ
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                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                            Kapur V.;
                                                                                                                                                                                                                                                                                                                       DB 2; Length 550;
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                                                                                                                                 Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017233, AAS04130.1; -; Genomic_DNA.
InterPro, IPR000030; Microbac_PPR.
Complete proteome.
SEQUENCE 550 AA, 54593 MW; E974C5075A847ECE CRC64;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                     21.6%; Score 408.5; DB 2; 32.0%; Pred. No. 5.2e-15; ive 48; Mismatches 162;
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4atches 121; Conservative
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e : 166 secs
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STRAIN=k10;
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Best Local S
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January 5, 2006, 16:44:30; Search time 40 Seconds (without alignments) 892.410 Million cell updates/sec
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1892
1 MITMLWHAMPPELNTARLMA......PLAQEREBDDEDDWDBEDDW 371
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

hypothetical prote probable PPB prote PPB prote PPB PPB prote probable PPB prote probable PPB prote probable PPB prote probable PPB prote PPB probable PPE Description G70802 T10033 E70857 D70857 E70831 G70929 H70931 H70750 B70931 F70513 F70513 F70513 F70513 D70922 D70922 G70925 F70560 T45392 % Query Match Length DB 22222.8 22222.8 22222.9 22222. 1878 527 430.5 4430.5 383.5 383.5 379.5 376.5 374 373 373 365.5 365.5 365.5 360.5 350.5 350.5 350.5 Score Result

319.5 16.9 394 2 G70881 318 16.8 409 2 B706881 315 16.8 409 2 B70608 315 16.7 539 2 A70899 312 16.5 402 2 H70741 311.5 16.5 501 2 C46930 303 15.0 538 2 C70780 299.5 15.8 443 2 C70780 299 15.8 443 2 C70780 287.5 15.2 409 2 A70647 287.5 15.2 582 2 F70675 277 14.4 655 2 A70931
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ALIGNMENTS

RESULT 1 G70802 probable PPI Cybate: 17-1 AyTitle: De AyReference AyReference AyReference AyRolecule AYRO	RESULT 1 G70802 probable PPE protein C;Species: Mycobacter C;Date: 17-Jul-1998 # C;Accession: G70802 R;Cole, S.T.; Brosch, R;Authors: S.T.; Brosch, Rajandream, M.A.; Rog Nature 393, 537-54, A;Authors: Sqares, R. A;Title: Deciphering A;Reference number: A A;Title: Deciphering A;Reference number: A A;Residues: preliminary A;Mocecule type: DNA A;Residues: 1-368 «CC A;Cross-references: U A;Resperimental source C;Genetics: A;Genetics:	RESULT 1 G70802 Cybobacterium tuberculosis (strain H37RV) Cycloside: Mycobacterium tuberculosis Cybote: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 Connor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Nature 139; 537-54, 1998 Asalancem, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Astathors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. Astathors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. Astathors: A
Query Ma Best Loc Matches	al 36) 99.3%; Score 1878; DB 2; Length 368; Similarity 100.0%; Pred. No. 1.9e-104; 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Ор	61	SDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLT 120
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අු	181	STTNPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFSQVGGTG 240
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ор	241	ggnpadeeaaqmgligteplsnhplaggsgpsagagliraeslpgaggsltrtplmsqli 300
È	304	EKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDED 363
QQ	301	EKPVAPSVMPAAAGSSATGGAAFVGAGAMGQGAQSGSTRPGLVAPAPLAQEREEDDED 360

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364 DWDEEDDW 371

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hypothetical probable PPE proba

A70646 B87158 C70582 S77655 B70932

344.5 344.5 343.5 331 325.5 325.5 323.5

B70625 E70929

A70504

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submitted to the EMBL Data Library, April 1991
A;Reference number: $21832
A;Reference number: $21834
A;Molecule type: DNA
A;Residues: 160-293, 'Aspr@anv@gv@rccgsgccswv@rgggglgrsacgccgcwragg', 338-354,' VGVGGGAGSREH
A;Notes: telerences: UNIPARC:UPI0000179FE0; EMBL:X59271
A;Note: the authors identified this protein as dihydrofolate reductase
C;Genetics:
A;Gene: PPE
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70836
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Davies, R.; Davin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: D70836
A;Accession: D7084
A;Accession: D708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 22.8%; Score 430.5; DB 2; Best Local Similarity 33.2%; Pred. No. 1.5e-18; Matches 132; Conservative 45; Mismatches 158;
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Best Local Similarity 33.3<sup>†</sup>
Matches 134<sup>†</sup>, Conservative
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FRESULT 3

Frobable PPE protein - Mycobacterium tuberculosis (atrain H37RV)

NyAlternate names: dihydrofolate reductase [misidentification]

Cipperdes: Mycobacterium tuberculosis

Cipperdes: Mycobacterium tuberculosis

Cipperdes: Mycobacterium tuberculosis

Cipperdes: Nycobacterium tuberculosis

Cipteres: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 09-Jul-2004

Cipteres: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 09-Jul-2004

Cipteres: Nycobacterium tuberculosis

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamiln, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.

A; Mature 393, 537-544, 1998

A; Reference number: A70500; MUID:98295987; PMID:9634230

A; Reference number: A70500; MUID:98295987; PMID:9634230

A; References: UNIPPOT:P1500; UNIPPRC:UP10000036B8C; GB:AL021287; GB:AL123456; NID

A; Residues: L-434 <COL>
A; Residues: UNIPPARC:UP1000016532D; GB:AL021287; GB:AL123456; NID

A; Residues: 1-81, P' <COL>
A; Residues: UNIPPARC:UP1000016532D; GB:AL021287; GB:AL123456; NID:G3261508; PIDN:
A; Residues: 1-81, P' <COL>
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A; Residues: 1-81, P' <COL>
A; Residues: 1-81, P' <COL>
A; Residues: UNIPPARC:UP1000016532D; GB:AL021287; GB:AL123456; NID:G3261508; PIDN:
A; Restrancial source: strain H37RV
A; Residues: UNIPPARC:UP1000016532D; GB:AL021287; GB:AL123456; NID:G3261508; PIDN:
A; Restrancial source: strain H37RV
A; Residues: UNIPPARC:UP1000016532D; GB:AL021287; GB:AL123456; NID:G3261508; PIDN:
A; Restrancial source: strain H37RV
A; Restrancial 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 LISQVNQFIQMISGFSAALPSTQVLQ-----QTVGQVAE-----LARPMQQVKSLFT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWTPLMTQPQLIDKSIAPEPRQRVMLP------PWAAGSPGHNAQDGGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIDSTGYYTSAQRGDTESAHRIGLFGASTLSSHPLVGITGTTTDTRLLCAESLPSASGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SQ--STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTSLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.9%; Score 527; DB 2; Length 305 Best Local Similarity 45.1%; Pred. No. 1.9e-24; Matches 134; Conservative 31; Mismatches 78; Indels
                                                                                                                        DWDEEDDW 368
                                                                                                                        361
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probable PPB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
S;Connor, R.; Barsch, R.; Parkhill, J.; Garnler, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Selton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-393 cCOL>
A;Cross-references: UNIPROT:053939; UNIPARC:UPI00001652AA; GB:AL022021; GB:AL123456; NI:A;Residues: PPB
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70852
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Bavies, R.; Devlin, K.; Feltwell, T.; Gencles, S.; Hamlin, N.; Holroyd, Espaineam, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 MAEAVAPYVAMMSAAAAQAEQAATQARAAAAREAAFAATVPPPLIAANRASLMQLISTN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 VFGONTSAIAAABAQYG-EMWAQDSAAMYAYAGSSASASAVTPFSTPPQIANPTAQGTQA 183
FDWPTHMLQLATWLAENPQLLVAALTPAISGLGAVSGLAGLTGLVPQPPVVPAPAPDAVV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAWTGGGSDK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 FGTPNFPTSISALLTDLÓPYASFFYNTEGLPYFSIGMGNNFIQSAKTLGLIGSAAPAAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 ALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLTATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GASQST-TNPIFGMPSPGSSTPVGQLPPAATQTLGQ--LGEMSGPMQQLTQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 393;
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20.3%; Score 383.5; DB 2; Length Best Local Similarity 32.0%; Pred. No. 8.2e-16;
Matches 131; Conservative 38; Mismatches 156; Indels
                                                     PSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAP 350
                                                                                                        PTVLPLAGTATPTTAPASAPAAGA-APGPPAGTATATSASVP 376
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Davies, R.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Davies, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G., A;Attler: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70831
A;Reterence number: A70500; MUID:98295987; PMID:9634230
A;Reterence number: A70500; MUID:98295987; PMID:9634230
A;Reterence prominary: nucleic acid sequence not shown; translation not shown A;Residues: 1-518 <COL>
A;Coss-references: UNIPROT:053738; UNIPARC:UPI0000004FC2; GB:AL021932; GB:AL123456; NIC A;Genetics: A;Gene: PPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATNFFGINTIPIALTEMDYFIRMWQALAMEVYQ--AETAVNTLFEKLEPMASILDPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAESFAAACLPYLSWLTQASADCAAAARLEAVTAAYAAALVAMPTLAELAANHATHGAM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 PAGLGLGLAAIAFLPIVLAPAVIPPAS----TPLAAAAV---AAGSVWPAV---SMAVT 328
                                                        120 AVLTAINFEGINTIPIALTEMDYFIRWMNQAALAMBVYQAET-AVNTLFEKLEPMASILD 178
                                                                                                                                                     121 TVLVATNPFGINTIPITLINEADY-VRMWIQAAAVMGLYQAASGAALASAPRTVPAPTVMN 179
                                                                                                                                                                                                                                 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLAGGSGPSAGAGL---LRAESLPGAGGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MIWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAWTGG 62
                   TGGGSDKALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASO-STINPIFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPLQQVTS---LF
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                                                                                                                                                                                                                                 PGASQSTINPIFGMPSPGSSTP-----VGQLPPAATQTLGQLGEMSGPMQQ-----
                                                                                                                                                                                                                                                                                                                                            ----LFSQVGGTGGGNPADEEAAQMGLLGTSPLSNH
                                                                                                                                                                                                                                                                                                                                                                              180 PGGGAAST-----VGAVNPWQWLLALLQQLWNAYTGFYGWMLQLIWQFLQDPIGNSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 GAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREEDDEDDW 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTAGAATPAAGAAPSAGAAPAAPATASFAYAVGGSGDW 370
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Matches 119; Conservative
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Cispecies: Mycobacterium tuberculosis

Cispecies: Millosis (R.; Bergell, R.; Peltwell), T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 333, 537-544, 1998

A;Authors: Sqares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Sqares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Sqares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Sqares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Procession: H70531

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Accession: H70931

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Accession: 1-403 <COL>
A;Cross-references: UNIPROT: O53956; UNIPARC: UPI0000004FB0; GB: AL022021; GB: AL123456; NIC

C;Genetics:
A;Genetics:
A;Genetics:
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A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge: A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70835
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-536 <COL>
A;Cross-references: UNIPARC:UPI0000003AF4; GB:AL021930; GB:AL123456; NID:g3261524; IA;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
A;Gene: PPB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAYVAAHAPYLAWIMRASETSAEAAARHETVAAAYTTÄVAAMPTLVELAANHTLHGVLV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SQVGGTGGGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAE 284
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                                                                                                                                                                                                                                                                                                          41; Mismatches 152; Indels 118;
                                                                                                                                                                                                                                                             Length 536;
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                                                                                                                                                                                                                                                      10.2%; Score 382; DB 2; al Similarity 30.1%; Pred. No. 1.4e-15; 134; Conservative 41; Mismatches 152:
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20.1%; Score 379.5; DB 2; 32.2%; Pred. No. 1.5e-15; tive 46; Mismatches 151;

Query Match Best Local Similarity 32.2* Matches 132; Conservative

Length 403;

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70750
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atcession: H70750
A;Accession: H70750
A;Access
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MPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSL-GEAWTGGGSDKA
                                                 LAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLTATNF
                                                                                                                                                                                                        ----ASILDPGASQSTINP-IFGMPS--PG-SSTPVGQLPPAATQTLGQLGEMSGPMQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 LGGTPMVAPPAVAAGMPFGTMGGQGFGRAVPQYGFRPNFVARPPAA 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 TQPLQQVTSLFSQVGGTGGGNPADEEAAQMGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.34
Matches 119; Conservative
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                                                                                                                                                                                                                                                                                                                       128
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Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, F.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230

A.Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-350 <COL>
A.COL>
A.COSS-references: UNIPROT:053940; UNIPARC:UPI00001652AB; GB:AL022021; GB:AL123456; NIIASCOSS-references: Strain H37Rv
C;Genetics:
A;Gene: PPB
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-01-1998 #sequence_revision 17-01-1998 #text_change 22-Oct-1999
C;Date: 17-01-1998 #sequence_revision 17-01-1998 #text_change 22-Oct-1999
C;Dates: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C;Connor, R.; Davies, R.; Devili, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295997; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 GGSLIRTPLMSQLIEKPVAPSVMPAAAGSSATGGAAPVGAGAMGOG---AQSGGST--- 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPGINTIPIALTEMDYFIRMWNQAALAMEVYQAETAVNTLFEKLEPMAS-----I 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 LDPGASQSTTNP-----IFGMPSPGSSTPVGQLPPAATQTLGQLGEMSGPMQQLTQPL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AQAVASVSWPNPNDWWLVRLLGSITPTERTTIVRL-----LGGSYLATGMARFLTSIA 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AMPPELNTARIAMGAGPAPMLAAAGWQTLSAALDAQAVELTARINSL-GEAWTGGGSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 ALAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPELAANHITQAVLTATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches 149; Indels
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Pred. No. 4.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 32.9%; Pred. No. 2.6e-15;
Matches 124; Conservative 42; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :: :| |
333 AHRYGFRHSVITRSPSA 349
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28.9%;
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Best Local Similarity
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70331
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Daviss, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70931
A;Accession: B70931
A;Accession: UNIPROT:053950; UNIPARC:UPI00000D5E6B; GB:AL022021; GB:AL123456; NIE
A;Residues: 1-423 <COL>
A;Cons-references: UNIPROT:053950; UNIPARC:UPI0000D5E6B; GB:AL022021; GB:AL123456; NIE
A;Experimental source: strain H37RV
C;Genetics: PPE
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                              240 YASYGLLLPPFPTPTLSALTALSALIHLINLPPAGLLPIAAALG-----PGDQWGANLA 293
                                                                                                                                              LLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGAG--GSLTRTPLMSQLIEKPVAPSVMPA 314
                                                                                                                                                                                        probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 MPPELNTARLMAGAGPAPMLAAAAGWQTLSAALDAQAVELTARLNSLGEAWTGGGSDKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch
al Similarity 31.7%; Pred. No. 2.5e-15;
128; Conservative 35; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALHTPILGSEGL-----GGGSVSAGIGRAGLVGKLSVPQGW----
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                                                                                                                                                                                                                                                                                                                                                                 348 PKAGTKSPDTAADTLATA-----GAARPGL 372
                                                                                                                                                                                                                                                                                                315 AAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGL 347
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C;Accession: A70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Cross-references: UNIPROT:P95247; UNIPARC:UPI00000D5E93; GB:ZB3860; GB:AL123456; NID:g A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 -----MASILDPGASQSTTNPIFGMPS--PGSSTPVGQLPPAATQTLGQLGE-----MS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GAQLICMAISVSAALSPIAEGAVEGVPAVVAAAOSVAAGLPVDAALQVGQAAAYPASMLI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 LAAATPMVVWLQTASTQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLTATNF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AGAAAPYVGWISAAAGQAELSAGQATAAATAFBAALAATVHPAAVTANRVLLGALVATNI 127
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